

RAW SEQUENCE LISTING

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Information Center (STIC) no errors detected.

Application Serial Number: 10/593,841
Source: IFWP
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IFWP

RAW SEQUENCE LISTING

DATE: 10/03/2006

PATENT APPLICATION: US/10/593,841

TIME: 08:45:28

Input Set : A:\9237.21WO Sequence Listing CRF.TXT

Output Set: N:\CRF4\10032006\J593841.raw

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3 <110> APPLICANT: University of Texas at San Antonio
4     Louisiana State University Health Sciences Center
5     Heidner, Hans Walter
6     Klimstra, William Brown
7     Ryman, Katherine Diana
9 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS COMPRISING PROTEIN L IMMUNOGLOBULIN
10    BINDING DOMAINS FOR CELL-SPECIFIC TARGETING
12 <130> FILE REFERENCE: 9237.21WO
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/593,841
C--> 14 <141> CURRENT FILING DATE: 2006-09-22
14 <160> NUMBER OF SEQ ID NOS: 27
16 <170> SOFTWARE: PatentIn version 3.2
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 2657
20 <212> TYPE: DNA
21 <213> ORGANISM: Peptostreptococcus magnus
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27 <223> OTHER INFORMATION: protein L
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36 <222> LOCATION: (820)..(1035)
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39 <220> FEATURE:
40 <221> NAME/KEY: repeat_unit
41 <222> LOCATION: (1036)..(1251)
42 <223> OTHER INFORMATION: PpL3
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45 <221> NAME/KEY: repeat_unit
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47 <223> OTHER INFORMATION: PpL4
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50 <221> NAME/KEY: repeat_unit
51 <222> LOCATION: (1468)..(1686)
52 <223> OTHER INFORMATION: PpL5
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59 tgttgatcac cctttttggg taaacaataa ctaaggaatg gcaatatatt tgcttgaaa 180
61 cgaatttgat ttaaatagca ttgaatgcaa aaaaatttaa aaggaggaga caaattccac 240
63 ccttattaga agggaagttt ccattgtcat gatattatga aaattaataa gaaattatta 300
65 atg gct gca ctt gca ggt gca att gta gta aca ggt gga gta gga tct 348
66 Met Ala Ala Leu Ala Gly Ala Ile Val Val Thr Gly Gly Val Gly Ser
67 1 5 10 15
69 tac gca gct gat gaa cct att gat ctt gaa aaa ctt gaa gaa aaa agg 396
70 Tyr Ala Ala Asp Glu Pro Ile Asp Leu Glu Lys Leu Glu Glu Lys Arg
71 20 25 30
73 gat aaa gaa aat gta gga aat tta cca aaa ttc gat aat gaa gtt aaa 444
74 Asp Lys Glu Asn Val Gly Asn Leu Pro Lys Phe Asp Asn Glu Val Lys
75 35 40 45
77 gat ggt tca gaa aat cca atg gct aaa tat cca gat ttc gat gat gaa 492
78 Asp Gly Ser Glu Asn Pro Met Ala Lys Tyr Pro Asp Phe Asp Asp Glu
79 50 55 60
81 gcc agt aca aga ttt gaa aca gaa aac aat gaa ttt gaa gaa aaa aaa 540
82 Ala Ser Thr Arg Phe Glu Thr Glu Asn Asn Glu Phe Glu Glu Lys Lys
83 65 70 75 80
85 gtt gtt tct gat aac ttt ttt gat caa tca gaa cat ccg ttt gta gaa 588
86 Val Val Ser Asp Asn Phe Phe Asp Gln Ser Glu His Pro Phe Val Glu
87 85 90 95
89 aat aaa gaa gaa aca cca gaa aca cca gaa act gat tca gaa gaa gaa 636
90 Asn Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser Glu Glu Glu
91 100 105 110
93 gta aca atc aaa gct aac cta atc ttt gca aat gga agc aca caa act 684
94 Val Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser Thr Gln Thr
95 115 120 125
97 gca gaa ttc aaa gga aca ttt gaa aaa gca aca tca gaa gct tat gcg 732
98 Ala Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu Ala Tyr Ala
99 130 135 140
101 tat gca gat act ttg aag aaa gac aat gga gaa tat act gta gat gtt 780
102 Tyr Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val
103 145 150 155 160
105 gca gat aaa ggt tat act tta aat att aaa ttt gct gga aaa gaa aaa 828
106 Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys
107 165 170 175
109 aca cca gaa gaa cca aaa gaa gaa gtt act att aaa gca aac tta atc 876
110 Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile
111 180 185 190
113 tat gca gat gga aaa aca caa aca gca gaa ttc aaa gga aca ttt gaa 924
114 Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu
115 195 200 205
117 gaa gca aca gca gaa gca tac aga tat gca gat gca tta aag aag gac 972
118 Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu Lys Lys Asp
119 210 215 220
121 aat gga gaa tat aca gta gac gtt gca gat aaa ggt tat act tta aat 1020
122 Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn
123 225 230 235 240
125 att aaa ttt gct gga aaa gaa aaa aca cca gaa gaa cca aaa gaa gaa 1068

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126	Ile	Lys	Phe	Ala	Gly	Lys	Glu	Lys	Thr	Pro	Glu	Glu	Pro	Lys	Glu	Glu	
127					245					250					255		
129	gtt	act	att	aaa	gca	aac	tta	atc	tat	gca	gat	gga	aaa	aca	caa	aca	1116
130	Val	Thr	Ile	Lys	Ala	Asn	Leu	Ile	Tyr	Ala	Asp	Gly	Lys	Thr	Gln	Thr	
131				260					265					270			
133	gca	gaa	ttc	aaa	gga	aca	ttt	gaa	gaa	gca	aca	gca	gaa	gca	tac	aga	1164
134	Ala	Glu	Phe	Lys	Gly	Thr	Phe	Glu	Glu	Ala	Thr	Ala	Glu	Ala	Tyr	Arg	
135				275					280					285			
137	tat	gct	gac	tta	tta	gca	aaa	gaa	aat	ggg	aaa	tat	aca	gta	gac	gtt	1212
138	Tyr	Ala	Asp	Leu	Leu	Ala	Lys	Glu	Asn	Gly	Lys	Tyr	Thr	Val	Asp	Val	
139		290						295				300					
141	gca	gat	aaa	ggg	tat	act	tta	aat	att	aaa	ttt	gct	gga	aaa	gaa	aaa	1260
142	Ala	Asp	Lys	Gly	Tyr	Thr	Leu	Asn	Ile	Lys	Phe	Ala	Gly	Lys	Glu	Lys	
143	305					310					315				320		
145	aca	cca	gaa	gaa	cca	aaa	gaa	gaa	gtt	act	att	aaa	gca	aac	tta	atc	1308
146	Thr	Pro	Glu	Glu	Pro	Lys	Glu	Glu	Val	Thr	Ile	Lys	Ala	Asn	Leu	Ile	
147				325					330					335			
149	tat	gca	gat	gga	aaa	act	caa	aca	gca	gag	ttc	aaa	gga	aca	ttt	gca	1356
150	Tyr	Ala	Asp	Gly	Lys	Thr	Gln	Thr	Ala	Glu	Phe	Lys	Gly	Thr	Phe	Ala	
151				340					345				350				
153	gaa	gca	aca	gca	gaa	gca	tac	aga	tac	gct	gac	tta	tta	gca	aaa	gaa	1404
154	Glu	Ala	Thr	Ala	Glu	Ala	Tyr	Arg	Tyr	Ala	Asp	Leu	Leu	Ala	Lys	Glu	
155				355				360				365					
157	aat	ggg	aaa	tat	aca	gca	gac	tta	gaa	gat	ggg	gga	tac	act	att	aat	1452
158	Asn	Gly	Lys	Tyr	Thr	Ala	Asp	Leu	Glu	Asp	Gly	Gly	Tyr	Thr	Ile	Asn	
159		370					375				380						
161	att	aga	ttt	gca	ggg	aag	aaa	gtt	gac	gaa	aaa	cca	gaa	gaa	aaa	gaa	1500
162	Ile	Arg	Phe	Ala	Gly	Lys	Lys	Val	Asp	Glu	Lys	Pro	Glu	Glu	Lys	Glu	
163	385					390					395				400		
165	caa	gta	aca	att	aaa	gaa	aat	ata	tat	ttt	gaa	gat	gga	aca	gta	caa	1548
166	Gln	Val	Thr	Ile	Lys	Glu	Asn	Ile	Tyr	Phe	Glu	Asp	Gly	Thr	Val	Gln	
167				405					410				415				
169	act	gca	aca	ttt	aaa	gga	aca	ttt	gca	gaa	gca	aca	gca	gaa	gca	tac	1596
170	Thr	Ala	Thr	Phe	Lys	Gly	Thr	Phe	Ala	Glu	Ala	Thr	Ala	Glu	Ala	Tyr	
171				420					425				430				
173	aga	tat	gca	gat	ttg	tta	tca	aaa	gaa	cat	ggg	aaa	tac	aca	gca	gac	1644
174	Arg	Tyr	Ala	Asp	Leu	Leu	Ser	Lys	Glu	His	Gly	Lys	Tyr	Thr	Ala	Asp	
175			435					440				445					
177	ttg	gaa	gat	ggg	gga	tac	act	atc	aac	att	aga	ttt	gct	gga	aaa	gaa	1692
178	Leu	Glu	Asp	Gly	Gly	Tyr	Thr	Ile	Asn	Ile	Arg	Phe	Ala	Gly	Lys	Glu	
179		450					455				460						
181	gaa	cca	gaa	gaa	aca	cca	gaa	aaa	cca	gaa	gta	caa	gac	gga	tat	gca	1740
182	Glu	Pro	Glu	Glu	Thr	Pro	Glu	Lys	Pro	Glu	Val	Gln	Asp	Gly	Tyr	Ala	
183	465					470				475			480				
185	tca	tac	gaa	gaa	gct	gaa	gca	gca	gct	aaa	gaa	gct	ttg	aaa	aat	gat	1788
186	Ser	Tyr	Glu	Glu	Ala	Glu	Ala	Ala	Ala	Lys	Glu	Ala	Leu	Lys	Asn	Asp	
187				485					490			495					
189	gat	gta	aat	aaa	tca	tat	act	att	aga	caa	ggg	gca	gat	gga	aga	tat	1836
190	Asp	Val	Asn	Lys	Ser	Tyr	Thr	Ile	Arg	Gln	Gly	Ala	Asp	Gly	Arg	Tyr	

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193 tac tat gta tta tca cca gta gaa gct gaa gaa gaa aaa cca gaa gca      1884
194 Tyr Tyr Val Leu Ser Pro Val Glu Ala Glu Glu Glu Lys Pro Glu Ala
195          515          520          525
197 caa aat gga tat gca aca tac gaa gaa gca gaa gca gca gct aag aaa      1932
198 Gln Asn Gly Tyr Ala Thr Tyr Glu Glu Ala Glu Ala Ala Ala Lys Lys
199          530          535          540
201 gct ttg gaa aat gat cca atc aat aaa tct tac agc ata aga caa ggt      1980
202 Ala Leu Glu Asn Asp Pro Ile Asn Lys Ser Tyr Ser Ile Arg Gln Gly
203 545          550          555          560
205 gca gat gga aga tac tac tat gta tta tca cca gta gaa gct gaa act      2028
206 Ala Asp Gly Arg Tyr Tyr Tyr Val Leu Ser Pro Val Glu Ala Glu Thr
207          565          570          575
209 cct gaa aaa cca gta gaa cca tca gaa cca tca aca cca gat gta cca      2076
210 Pro Glu Lys Pro Val Glu Pro Ser Glu Pro Ser Thr Pro Asp Val Pro
211          580          585          590
213 tca aac cca tca aat cca tca aca cca gat gtt cca tca act cct gat      2124
214 Ser Asn Pro Ser Asn Pro Ser Thr Pro Asp Val Pro Ser Thr Pro Asp
215          595          600          605
217 gta cca tca aat cct tca act cca gaa gtt cct tca aac cca tca act      2172
218 Val Pro Ser Asn Pro Ser Thr Pro Glu Val Pro Ser Asn Pro Ser Thr
219          610          615          620
221 cct ggt aat gaa gaa aaa cct ggt aac gaa caa aaa cct ggt aac gaa      2220
222 Pro Gly Asn Glu Glu Lys Pro Gly Asn Glu Gln Lys Pro Gly Asn Glu
223 625          630          635          640
225 caa aaa cct ggt aac gaa caa aaa cct ggt aat gaa caa aaa cct ggt      2268
226 Gln Lys Pro Gly Asn Glu Gln Lys Pro Gly Asn Glu Gln Lys Pro Gly
227          645          650          655
229 aat gaa caa aaa cca gac caa cct tca aaa cca gaa aaa gaa gaa aat      2316
230 Asn Glu Gln Lys Pro Asp Gln Pro Ser Lys Pro Glu Lys Glu Glu Asn
231          660          665          670
233 ggt aag ggt gga gta gat tct cca aag aaa aaa gaa aaa gct gca tta      2364
234 Gly Lys Gly Gly Val Asp Ser Pro Lys Lys Lys Glu Lys Ala Ala Leu
235          675          680          685
237 cca aaa gct ggt agc gaa gct gaa atc tta aca tta gca gca gct tca      2412
238 Pro Lys Ala Gly Ser Glu Ala Glu Ile Leu Thr Leu Ala Ala Ala Ser
239          690          695          700
241 tta tca agc gtt gca ggt gct ttc att tca ctt aaa aaa cgt aaa taa      2460
242 Leu Ser Ser Val Ala Gly Ala Phe Ile Ser Leu Lys Lys Arg Lys
243 705          710          715
245 ttaatcttag ataaaaaata gattaatcta aaaaaatggg actttttataa gtcccatTTT      2520
247 tgattgcaat gaaactgata caaaaaatgt atcagttttt tcattttacgc ttattttcct      2580
249 gtgagtatgt ccaagtttgt cgtataatca tctatcaaaa gcctggcgag ttctgctttt      2640
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254 <210> SEQ ID NO: 2
255 <211> LENGTH: 719
256 <212> TYPE: PRT
257 <213> ORGANISM: Peptostreptococcus magnus
259 <400> SEQUENCE: 2

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261 Met Ala Ala Leu Ala Gly Ala Ile Val Val Thr Gly Gly Val Gly Ser
262 1 5 10 15
265 Tyr Ala Ala Asp Glu Pro Ile Asp Leu Glu Lys Leu Glu Glu Lys Arg
266 20 25 30
269 Asp Lys Glu Asn Val Gly Asn Leu Pro Lys Phe Asp Asn Glu Val Lys
270 35 40 45
273 Asp Gly Ser Glu Asn Pro Met Ala Lys Tyr Pro Asp Phe Asp Asp Glu
274 50 55 60
277 Ala Ser Thr Arg Phe Glu Thr Glu Asn Asn Glu Phe Glu Glu Lys Lys
278 65 70 75 80
281 Val Val Ser Asp Asn Phe Phe Asp Gln Ser Glu His Pro Phe Val Glu
282 85 90 95
285 Asn Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser Glu Glu Glu
286 100 105 110
289 Val Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser Thr Gln Thr
290 115 120 125
293 Ala Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu Ala Tyr Ala
294 130 135 140
297 Tyr Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val
298 145 150 155 160
301 Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys
302 165 170 175
305 Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile
306 180 185 190
309 Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu
310 195 200 205
313 Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu Lys Lys Asp
314 210 215 220
317 Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn
318 225 230 235 240
321 Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu
322 245 250 255
325 Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr
326 260 265 270
329 Ala Glu Phe Lys Gly Thr Phe Glu Ala Thr Ala Glu Ala Tyr Arg
330 275 280 285
333 Tyr Ala Asp Leu Leu Ala Lys Glu Asn Gly Lys Tyr Thr Val Asp Val
334 290 295 300
337 Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys
338 305 310 315 320
341 Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile
342 325 330 335
345 Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Ala
346 340 345 350
349 Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Glu
350 355 360 365
353 Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr Thr Ile Asn
354 370 375 380
357 Ile Arg Phe Ala Gly Lys Lys Val Asp Glu Lys Pro Glu Glu Lys Glu

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VERIFICATION SUMMARY

PATENT APPLICATION: **US/10/593,841**

DATE: 10/03/2006

TIME: 08:45:29

Input Set : **A:\9237.21WO Sequence Listing CRF.TXT**

Output Set: **N:\CRF4\10032006\J593841.raw**

L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date